**2023 and 2024 ODFW Columbian White-tailed Deer Analysis Summary-North Bank Wildlife Area within Melrose WMU**

***2023 Columbian white-tailed deer***

We analyzed 144 dog-collected samples from the North Bank Wildlife Area in the Melrose WMU. Of the 144 samples, we were able to identify 33 Columbian white-tailed deer via sequencing and depending on the alleles seen for locus T159S, the remaining 111 were black-tailed deer.

*Individual matching analyses:*  
The probability of identity is the probability that two unrelated individuals will have the same genotype (and thus be genetically indistinguishable) using these markers, while the probability of identity for siblings is the probability that two related individuals, whether a parent-offspring pair or siblings, will have the same genotype. As per study goals, we set a threshold of probability of identity (PID) <0.001 and probability of identity for siblings (PIDsibs) <0.05. We calculated these values for the North Bank Wildlife area in the Melrose WMU using seven microsatellite markers.

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| **# of loci** | **PID** | **PIDsibs** |
| 7 | 3.8x10-4 | 2.4x10-2 |
| 6 | 8.9x10-4 | 3.6x10-2 |
| 5 | 1.9x10-3 | 5.3x10-2 |
|  |  |  |

Based on the PID and PIDsibs values, a minimum of six loci per individual sample of the Columbian white-tailed deer were needed for the North Bank Wildlife Area in the Melrose WMU in 2023. Samples that worked at fewer than six markers were excluded from recapture analyses.

Of the 33 Columbian white-tailed deer, 30 samples worked at 6 loci (91%). Out of the 30 white-tailed deer samples that worked at 6 loci, we identified 19 unique deer. Four deer were recaptured 2X (Deer #3, #4, #5 and #6 were sampled 3x) and the remaining 15 of the 19 unique deer were captured once (79%).

Of the 19 unique deer, 10 individuals were female, and 9 individuals were male.

***2024 Columbian white-tailed deer***

We analyzed 187 dog-collected samples from the North Bank Wildlife Area in the Melrose WMU. Of the 187 samples, we were able to identify 6 Columbian white-tailed deer via sequencing and depending on the alleles seen for locus T159S. The remaining 181 samples were black-tailed deer.

We retained the cutoff value calculated in 2023 given our very small sample size for 2024 (n=6) and therefore needed a minimum of six loci per individual sample for 2024. Those that worked at ≤6 markers were excluded from recapture analysis. Using this cutoff value, we had to remove one sample from 2024 that only worked at five loci but retained the remaining 5 samples that worked at ≥6 or more loci from 2024 and all 30 samples that worked at ≥6 or more loci from 2024, giving us a total of 35 samples to use for recapture analysis.

Of the 35 Columbian white-tailed deer samples that worked at ≥6 loci, we identified 22 unique deer. Four deer were recaptured 2X (Deer7\_2024, Deer8\_2024, Deer9\_2024 and Deer10\_2024 were sampled 3x) and the remaining 18 of the 22 unique deer were captured once (82%).

Of the 22 unique deer, 11 individuals were female, and 11 individuals were male.

We were able to make a match across the two years; 2023 NoB035\_2023 and 2024 NoB242\_2024 (Deer1\_2024).

When determining which samples were black-tailed deer vs Columbian white-tailed deer, there were two instances where the sample genotyped as one species, but the sequence data matched the alternative species. NoB247\_2024 genotyped as a black-tailed deer but its sequence matched Columbian white-tailed deer reference samples, where NoB258\_2024 genotyped as a Columbian white-tailed deer but its sequence data matched black-tailed deer reference samples. We sorted these two samples for species ID based on their genotype. So, NoB247\_2024 was grouped with the black-tailed deer samples and NoB258\_2024 was grouped with the Columbian white-tailed deer samples for the purpose of matching individuals and determining recaptures.

***Locus Information for Columbian white-tailed deer***

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| --- | --- | --- | --- | --- |
| **Locus** | **# of alleles** | **Allele size range (in bp)** | **Hobs** | **Hexp** |
| C273 | 2 | 142,170 | 0.500 | 0.381 |
| C89 | 5 | 171-187 | 0.382 | 0.751 |
| OdhE | 3 | 141-149 | 0.600 | 0.604 |
| SBTD05 | 3 | 113-141 | 0.156 | 0.459 |
| SBTD06 | 3 | 183-195 | 0.500 | 0.517 |
| T159s | 2 | 187,195 | 0.088 | 0.314 |
| T7 | 2 | 219,231 | 0.040 | 0.429 |

Many of these loci are out of Hardy-Weinberg most likely due to null alleles, allelic dropout or population substructure.